I claim:

1. A method of determining the sequence of a target nucleic acid sequence in a sample, comprising the steps of:

(a) providing a solid phase comprising particles having transponders, the particles having an oligonucleotide probe attached to a surface of the solid phase particles, the transponders having memory elements and an index number indicating sequence of the probe encoded on the transponders;

(c) contacting the solid phase with a sample to form a sample mixture;

(d) denaturing nucleic acids in the sample mixture;

(e) hybridizing the nucleic acids in the sample mixture, whereby target nucleic acid sequences hybridize to complementary probes;

(f) analyzing the solid phase to detect the presence of a label indicative of binding target nucleic acid to probes;

(g) decoding the data encoded on transponders using the dedicated read/write scanner to identify the sequence of the probes to which target nucleic acids are bound.

2. The method of claim 1, further comprising the step of analyzing the sequences of probes to which target nucleic acid bound to determine at least a portion of the sequence of the target nucleic acid.

3. The method of claim 1 wherein the label is bound to the target nucleic acid.

4. The method of claim 1 wherein the label is added after the annealing step through a chain extension reaction using DNA polymerase.

5. The method of claim 1 wherein the data comprises the sequence of the oligonucleotide probe deposited on solid phase.

6. The method of claim 1 wherein the data comprises characteristics of the sample.

7. A method of determining the sequence of target nucleic acid thought to contain a plurality of subsequences,

comprising the steps of:

(a) introducing into the sample at least two populations of solid phase particles, each particle having a transponder and having an oligonucleotide probe corresponding to one of the subsequences attached to its surface, a first population having a different oligonucleotide probe sequence than a second population and the transponders in the first population being encoded with a different identification than the transponders of the second population;

(b) denaturing the nucleic acids in the sample;

(c) hybridizing the nucleic acids in the sample, whereby target nucleic acid sequences hybridize to the oligonucleotide probes;

(c) analyzing the particles to detect a label indicating that target nucleic acid has bound to the probe; and

(d) decoding the transponder to determine the sequence of the probe.

8. The method of claim 7, wherein the solid phase comprises at least three populations of solid phase particles, each particle having a transponder and having an oligonucleotide probe corresponding to one of the subsequences attached to its surface, each of the three populations having a different oligonucleotide probe sequence and each of the populations being encoded with a different identification than the transponders of the second population.

9. The method of claim 7 wherein the surface of the particles is glass, latex or plastic.

10. The method of claim 7 wherein the oligonucleotide probe is single-stranded.

11. The method of claim 7, wherein the oligonucleotide probe is biotinylated and the particle is coated with a layer of streptavidin.

12. A kit for determining the sequence of target nucleic acids in a sample, comprising:

(a) at least one assay vessel, containing at least one solid phase particle having a transponder, and an oligonucleotide probe bound to a surface of the particle; and

(b) at least one label reagent.

13. The kit of claim 12, wherein the label reagent comprises a reagent that labels the target nucleic acid.

14. The kit of claim 12, wherein the label reagent comprises a labelled nucleoside for use in a chain extension reaction using DNA polymerase.

15. The kit of claim 12, further comprising:

(a) a sample diluent buffer solution; and

(b) an enzyme reaction buffer solution.